

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 11.9318 Seconds
(without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613B-2

Perfect score: 578
Sequence: 1 QDWLTFQKKHLNTRDVDCN.....TFCVTCENQAPVHFVGVC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	95.7	104	2 A39035	ribonuclease-relat
2	289	50.0	111	2 A27121	ribonuclease-relat
3	285.5	49.4	111	1 JX0120	ribonuclease-relat
4	269.5	46.6	111	2 JX0085	pancreatic ribonuc
5	149	25.8	119	2 S41111	pancreatic ribonuc
6	131	22.7	124	1 NRUI	pancreatic ribonuc
7	128	22.1	125	1 A32474	angiogenin [valida
8	125	21.8	128	1 NRCU	pancreatic ribonuc
9	125	21.6	124	1 NRMHK	pancreatic ribonuc
10	120	20.8	128	1 NRKS	pancreatic ribonuc
11	119.5	20.7	145	1 A35932	angiogenin precurs
12	119	20.6	128	1 NRGPB	pancreatic ribonuc
13	117	20.2	124	1 NRCB	pancreatic ribonuc
14	116	20.1	125	1 B43825	angiogenin - rabbi
15	116	20.1	128	1 NRY	pancreatic ribonuc
16	114	19.7	124	1 NRHP	pancreatic ribonuc
17	113	19.6	147	1 NRHUG	angiogenin precurs
18	112	19.4	124	1 NRBOB	pancreatic ribonuc
19	112	19.4	124	1 NRPQ	pancreatic ribonuc
20	112	19.4	124	2 J05560	pancreatic ribonuc
21	112	19.4	150	1 NRBO	pancreatic ribonuc
22	111.5	19.3	147	2 I52489	ribonuclease 4 (EC
23	111	19.2	124	2 S08549	ribonuclease - dom
24	111	19.2	128	1 NRHO	pancreatic ribonuc
25	111	19.2	128	1 NRPQ	pancreatic ribonuc
26	111	19.2	167	2 S20066	pancreatic-type ri
27	110.5	19.1	123	1 A43825	angiogenin - pig
28	110.5	19.1	155	2 UC6155	eosinophil-associa
29	109	18.9	124	1 NRSH	pancreatic ribonuc

30	109	18.9	124	1 NRPRH	pancreatic ribonuc
31	109	18.9	124	1 NRGA	pancreatic ribonuc
32	109	18.9	124	2 S07141	pancreatic ribonuc
33	108	18.7	124	1 NRWB	pancreatic ribonuc
34	108	18.7	124	1 NRGN	pancreatic ribonuc
35	107	18.5	124	1 NRGF	pancreatic ribonuc
36	106	18.3	156	2 JC6160	eosinophil-associa
37	105	18.2	124	1 NRDEO	pancreatic ribonuc
38	105	18.2	124	1 NRDM	pancreatic ribonuc
39	105	18.2	124	1 NRDM	pancreatic ribonuc
40	105	18.2	124	1 NRDM	pancreatic ribonuc
41	105	18.2	128	1 NRW2	pancreatic ribonuc
42	104	18.0	124	1 NRHY	pancreatic ribonuc
43	103	17.8	124	1 NRDE	pancreatic ribonuc
44	103	17.8	124	1 NRDE	pancreatic ribonuc
45	103	17.8	124	1 NREKN	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 95.7%; Score 553; DB 2; Length 104;
Best Local Similarity 95.2%; Pred. No. 1e-48;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY	1	QDWLTFQKKHLNTRDVDCNINMSTNLFHCKDKNTFIYSRPEPKAICGIIASKNVLT 60
DB	1	EDWLTFQKKHLNTRDVDCNINMSTNLFHCKDKNTFIYSRPEPKAICGIIASKNVLT 60
QY	61	SEFYLSDCNVTSRPFCKYKRLKSTNFCVTCENQAPVHFVGVC 104
DB	61	SEFYLSDCNVTSRPFCKYKRLKSTNFCVTCENQAPVHFVGVC 104

RESULT 2

A27121

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayan

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <RT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 50.0%; Score 289; DB 2; Length 111;
Best Local Similarity 48.6%; Pred. No. 4.1e-22;
Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY	1	QDWLTFQKKHLNTRDVDCNINMSTNLF---HCKDKNTFIYSRPEPKAICGIIASKN 56
DB	1	ENWATFQKKHLNTRDVDCNINMSTNLF---HCKDKNTFIYSRPEPKAICGIIASKN 59

QY 57 VLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
 Db 60 VLTSTRFQNLNCTRTSITPRPCPSRSRETNYICVKCENQVPHVFAGIGRC 110

RESULT 3

JX0120
 Ribonuclease-related stalic acid-binding lectin - Japanese frog
 C:Species: Rana japonica (Japanese frog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JX0120
 R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takeyanagi, J. Biochem. 108, 139-143, 1990
 A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
 A:Reference number: JX0120; MUID:91035319; PMID:2229005
 A:Accession: JX0120
 A:Molecule type: protein
 A:Residues: 1-111 <RAM>
 A:Experimental source: egg
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: lectin; pyroglutamic acid
 F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 49.4%; Score 285.5; DB 1; Length 111;
 Best Local Similarity 45.0%; Pred. No. 9.3e-22;
 Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

QY 1 QDWLTPOKKHLNTRDYDCNNIMSTNLF---HCKKNFTYSRPEPYKAICKGIATSKN 56
 Db 1 QNNAKQEKHNPNTSINCNITMDKSIYVGGCKEKERNFTIISATYKACISGASTNRN 60
 QY 57 VLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
 Db 61 VLTSTRFQNLNCTRTSITPRPCPSRSRETNYICVKCENRLLPVHVFAGIGRC 111

RESULT 4

JX0085
 Pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
 C:Species: Rana catesbeiana (bullfrog)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: JX0085
 R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, R. Biochem. 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
 A:Reference number: JX0085; MUID:90130374; PMID:2613682
 A:Accession: JX0085
 A:Molecule type: protein
 A:Residues: 1-111 <NIT>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: hydrolase; pyroglutamic acid
 F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F:10,35,104/Active site: His, Lys, His #status predicted
 F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 46.6%; Score 269.5; DB 2; Length 111;
 Best Local Similarity 43.2%; Pred. No. 3.8e-20;
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 1 QDWLTPOKKHLNTRDYDCNNIMSTNLF---HCKKNFTYSRPEPYKAICKGIATSKN 56
 Db 1 QNNAKQEKHNPNTSINCNITMDKSIYVGGCKEKERNFTIISATYKACISGASTNRN 60
 QY 57 VLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
 Db 61 VLTSTRFQNLNCTRTSITPRPCPSRSRETNYICVKCENRLLPVHVFAGIGRC 111

RESULT 5
 S4111
 Pancreatic ribonuclease - common iguana

C:Species: Iguana iguana (common iguana)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
 C:Accession: S4111
 R:Zhao, W.; Beintema, J.J.; Hofsteenge, J. Eur. J. Biochem. 219, 641-646, 1994
 A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
 A:Reference number: S4111; MUID:94139745; PMID:8307028
 A:Accession: S4111
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-119 <ZHA>
 C:Superfamily: pancreatic ribonuclease

Query Match 25.8%; Score 149; DB 2; Length 119;
 Best Local Similarity 30.7%; Pred. No. 5.5e-08;
 Matches 35; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

QY 1 QDWLTPOKKHLNTRDYDCNNIM---STNLFHCKDKNTFYSRPEPYKAICK-K 49
 Db 1 QDWSSFOKKHIDYDPTSSASNPAYCDLMORNLNPTKCKTRMTFVHASPSEIQVCGSG 60
 QY 50 GIATSKNVLTTSF-FYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFG 98
 Db 61 GTHYEDNLDSNPSFLTDCKNVGTAAPSCKTNGTPGTRIRIACENNOPVHF 114

RESULT 6

NROI
 Pancreatic ribonuclease (EC 3.1.27.5) - cuis
 N:Alternate names: RNase A
 C:Species: Galea musteloides (cuis)
 C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
 C:Accession: A00827
 R:Beintema, J.J.; Neuteboom, B. J. Mol. Evol. 19, 145-152, 1983
 A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the A:Reference number: A92957; MUID:87036770; PMID:6571219
 A:Accession: A00827
 A:Molecule type: protein
 A:Residues: 1-124 <BEI>
 A:Note: about one-third of the molecules lacked Ala-1
 C:Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:94/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 22.7%; Score 131; DB 1; Length 124;
 Best Local Similarity 30.6%; Pred. No. 3.7e-06;
 Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

QY 4 LTFQKKHLNTRDYDCNNIM---STNLFHCKDKNTFYSRPEPYKAICKGIATSKN 53
 Db 6 MKFQGHMDSDGHDPTNN--YCNEMVRRMTGRCCKPVVTEVHEPLEAVQAVC---S 59
 QY 54 SKNV-----LTTSEFYLSDCNVTSP---CKYKLLKSTNTFCVTCEN--QAPVH 97
 Db 60 QKNVPCKNQGTNYQSHSMRITDCRVTSKSKYPCNSYRMTQAKSTIVACEGTPSPVH 119

QY 98 F 98
 Db 120 F 120

RESULT 7
 A32474
 angiogenin [validated] - bovine
 N:Alternate names: angiogenesis factor
 N:Contans: ribonuclease (EC 3.1.27.-)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 15-Sep-2000
 C:Accession: A32474; S02001; A30044; S48212

R:Bond, M.D.: Strydom, D.J.
 Biochemistry 28, 6110-6113, 1989
 A:Title: Amino acid sequence of bovine angiogenin.
 A:Reference number: A32474; MUID:89375344; PMID:2775757
 A:Accession: A32474
 A:Molecule type: protein
 A:Residues: 1-125 <BON>
 A:Experimental source: Plasma
 R:Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
 FEBS Lett. 241, 41-45, 1988
 A:Title: The complete amino acid sequence of bovine milk angiogenin.
 A:Reference number: S02001; MUID:89065101; PMID:3197838
 A:Accession: S02001
 A:Molecule type: protein
 A:Residues: 1-125 <MAE>
 A:Experimental source: milk
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 Submitted to the Brookhaven Protein Data Bank, January 1995
 A:Reference number: A65065; PDB:1AG1
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms, residues 1-125
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
 A:Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
 A:Reference number: A58315; MUID:95224057; PMID:7708754
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
 Submitted to the Brookhaven Protein Data Bank, April 1996
 A:Reference number: A65709; PDB:1G10
 A:Contents: annotation: conformation by (1)H-NMR, residues 1-125
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
 Biochemistry 35, 8870-8880, 1996
 A:Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance spec
 A:Reference number: A58821; MUID:96280645; PMID:8688423
 A:Contents: annotation: conformation by (1)H-NMR
 R:Reisdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
 Eur. J. Biochem. 224, 811-822, 1994
 A:Title: Proton resonance assignments and secondary structure of bovine angiogenin.
 A:Reference number: S48212; MUID:95010071; PMID:7925406
 A:Contents: annotation: conformation by (1)H-NMR
 C:Function:
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation
 F:60-68/Region: receptor binding #status predicted
 F:14,41,115/Active site: His, Lys, His #status predicted
 F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 22.1%; Score 128; DB 1; Length 125;
 Best Local Similarity 34.0%; Pred. No. 7.5e-06;
 Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

QY 16 DVDCKNIMSTNLF--HCKDKNTFYSPREPVAICKGIILASKN-----VLTSEFYL 65
 DB 24 DEYCFPMKNNRLTRCKDKDRNTFHGKNKDIAICE-----DRNGQPYRGDLRIKSEFOI 79

QY 66 SDC--NWTSR-PCKYKLRKSTNFCVTCENQAPVHF 98
 DB 80 TICKHKGSSRPRCGRYATEDSRVIVGCGNGLPVHF 116

RESULT 8
 NRCU
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
 C:Accession: A00822
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
 A:Reference number: A90612; MUID:77065676; PMID:999896
 A:Accession: A00822
 A:Molecule type: protein

A:Residues: 1-128 <VAN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.8%; Score 126; DB 1; Length 128;
 Best Local Similarity 29.9%; Pred. No. 1.2e-05;
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 6 FORKH-----TTRVDCKNIM-STNLF--HCKDKNTFYSPREPVAICKGIILASKN 57
 DB 8 FERQHMDSRCPSTNPNYCNEMKSRNMTGCRCKPVTVEHDLADVAQV-----FOKNV 63

QY 58 L-----TTSEFYLDSCNVTSRP-----CKYKLRKSTNFCVTCENQ--APVHF 98
 DB 64 LCKNGQTCYQSNMNHITDCRVTNSDYPCNCSYRISOEKSIVVACGPNVYPVHF 120

RESULT 9
 NRRMK
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale
 N:Alternate names: RNase 1; RNase A
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
 C:Accession: A00818
 R:Emmens, M.; Welling, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.6%; Score 125; DB 1; Length 124;
 Best Local Similarity 28.6%; Pred. No. 1.5e-05;
 Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 4 LTFQKHLTMTROVD-----CNNIMSTNLF--HCKDKNTFYSPREPVAICKGIILASK 55
 DB 6 MKFQOHMDSGNSPCNNPNYCNQMMRRKMTGCRCKPVTVEHSLDYKAVC-----SQK 61

QY 56 NVL-----TTSEFYLDSCNVTSRP-----CKYKLRKSTNFCVTCENQ--APVHF 98
 DB 62 NVLCKNGRTNCEYNSPMHTTDCRQTSYKPRCAVKTQSKKHIIIVACGNGPYVYPVHF 120

RESULT 10
 NRRKS
 pancreatic ribonuclease (EC 3.1.27.5) - casiragua
 C:Species: Proechimys quadrata (casiragua)
 C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
 C:Accession: A00821
 R:Beintema, J.J.; Knol, G.; Martena, B.
 Biochim. Biophys. Acta 705, 102-110, 1982
 A:Title: The primary structures of pancreatic ribonucleases from African porcupine an
 A:Reference number: A90644; MUID:83000399; PMID:7115727
 A:Accession: A00821
 A:Molecule type: protein
 A:Residues: 1-128 <BEI>
 A:Note: residues 67-78 were positioned primarily by homology with other ribonucleases
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:21-34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84-40-95-58-110-65-72/Disulfide bonds: #status predicted

Query Match 20.6% Score 119; DB 1; Length 128;
Best Local Similarity 28.3%; Pred. No. 6,2e-05;
Matches 34; Conservative % 21; Mismatches 35; Indels 30; Gaps 7;

OY 4 LTFQKRL-----TNRDVCNNIM---STNLFHCKDKMTFTIYSRREPVAICKGIITAS 54
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 MKFDROMHDGSPSSNSNV-CNVMMIRRNATGCRCKPVTNFVHESLADYDAVC----FQ 60
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1998 #text_change 31-Mar-2000
C:Accession: A00820
R:van den Berg, A.: van den Hende-Timmer, L.: Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
E:12-41,119/Active site: His, Lys, His #status predicted
F:26-84-40-95-58-110-65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.2% Score 117; DB 1; Length 124;
Best Local Similarity 26.9%; Pred. No. 9.5e-05;
Matches 32; Conservative % 19; Mismatches 40; Indels 28; Gaps 6;

OY 4 LTFQKRL-----TNRDVCNNIM---STNLFHCKDKMTFTIYSRREPVAICKGIITASK 55
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 MKFDROMHDGSGSSTANANCENEMKRNMTOGICRVNFFVEPLADYDAVC----FOK 61
OY 56 NV-----LTTSFYLSDCNVTSRP---CKYKLKSTNTFCVTCENO--APVHF 98
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 NVPCKNGSCNOGSNSMHTDRCRLTNSKRYPCSYRTSRBNKKIIIVACEGNPVVPHF 120
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29833; B43825
R:Bond, M.D.; Stridom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A>Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discer
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29833
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-125 <BON>
A>Note: submitted to The Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglyutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.1% Score 116; DB 1; Length 125;
Best Local Similarity 31.2%; Pred. No. 0.00012;
Matches 24; Conservative % 13; Mismatches 32; Indels 8; Gaps 3;

